B10 d) diagnosing pathologies associated with said gene rearrangements when present.

17. (new) The method of claim 16, wherein the primers consist of 25 to 40 nucleotides.

SUB D7 18. (new) The method of claim 16, further comprising, labeling said PCR products, denaturing said labeled PCR products, and contacting the denatured labeled PCR products with a nucleotide sequence complementary to a fusion partner nucleotide sequence.

SUB F1 19. (new) The method of claim 18, wherein said complementary nucleotide sequence is a nucleotide probe covalently bonded on a support.

20. (new) The method of claim 18, wherein said probes are labeled and are present in solution.

21. (new) The method of claim 16, wherein one of the primers consists of a sequence containing a cassette of 40 to 60 nucleotides and 10 to 20 T nucleotides, and the second primer is a random repeat of nucleotides.

SUB D8 22. (new) The method of claim 16, wherein said part of the genome adjacent to the target gene is a fusion partner.

23. (new) The method of claim 22, comprising:

a) subjecting the patient's genome DNA or RNA to the action of a compound capable of cleaving or specifically inhibiting the DNA or RNA of the target gene, the fusion of which is to be detected,

b) performing said asymmetrical PCR,

c) reacting the PCR products thus obtained with two probes specific for each target gene, one being upstream, and the other one being downstream, and with probes complementary to known fusion partners,

a positive detection on the upstream probe and a negative detection on the downstream probe, corresponding to a rearrangement of the target genes, and a negative detection for the known partner genes corresponding to the absence of fusion with a known fusion partner, or alternatively,

d) reacting the PCR products with a plurality of probes bonded to a miniaturized support, and detecting hybridization of the probes with the PCR products, if any.

24. (new) The method of claim 22, wherein the rearrangement of the gene is a translocation associated with the MLL gene.

25. (new) The method of claim 24, comprising

a) the RT synthesis of a cDNA pool from the patient's RNA, using primers consisting of a cassette with 30 to 35 nucleotides with a sequence of 6 or 9 random nucleotides,

b) a PCR amplification using a first primer located on the MLL exon 5, as specific sense primer, the 3' primer being the same on each cycle and complementary to the oligonucleotide cassette used in the RT step.

26. (new) The method of claim 24, further comprising a second nested amplification cycle, using an internal sense primer with respect to the first MLL primer, where the 3' primer is the same on each cycle and complementary to the oligonucleotide cassette used in the RT step.

B10

27. (new) The method of claim 24, comprising, for detecting fusion transcripts,

a) contacting a probe specific for known MLL fusion partners, with denatured PCR products labeled with digoxygenine, in order to hybridize said probe with the PCR products where complementary bases are present,

b) contacting the hybridization products, when obtained, with anti-digoxygenine antibodies coupled with an enzyme and capable to react with the enzyme substrate by releasing a detectable product, and

SUB F1

c) contacting the probe/PCR product reactive mixture with the enzyme substrate, and

d) detecting the product so formed, if any.

28. (new) The method of claim 24, comprising, to detect new partner fusions of MLL gene,

a) subjecting total RNAs, before the RT-PCR, to the action of ribozymes MLL gene-specific,

b) reacting the PCR products with a first probe, complementary to MLL exon 5 sequence on the 3' end,

c) reacting the so-obtained PCR products with a second MLL gene-specific probe, located between the break points and ribozyme action site, and

d) reacting said PCR products with probes complementary to known partners.

SUB D10

29. (new) The method of claim 16, wherein said pathology is leukemia.

30. (new) The method of claim 16, wherein said pathology concerns solid tumors.

SUB B10 E21 31. (new) The method of claim 30, wherein said pathology concerns Ewing tumors.

32. (new) A kit for the diagnostic method according to claim 16, comprising reagents for carrying out the PCR and the detection step, and primers selected in the group consisting of primers specific for the target gene and random partners.

SUB D11 SUB E4 33. (new) A kit according to claim 32, further comprising agents capable of cleaving or blocking the gene of the polypeptidic nucleic acids or of the ribozymes.

SUB D12 34. (new) A kit according to claim 32, further comprising probes selected from the group comprising probes complementary to the target gene and probes complementary to known fusion partners.

SUB F1 35. (new) A kit according to claim 34, wherein said probes are bonded to plates.

36. (new) A kit according to claim 35, wherein said probes have a biotin group on their 5' end and are bonded to streptavidine coupled plates.

SUB E5 37. (new) A kit according to claim 34, wherein the probes are bonded to a miniaturized support.

38. (new) A kit according to claim 37 wherein the miniaturized support is a DNA chip.--

## REMARKS

Reconsideration is requested.

Claims 1-15 have been canceled, without prejudice. Claims 16-38 have been added and are pending.